9

```
 1
 2
 3
 4                          SEQUENCE LISTING
 5
 6   (1)   GENERAL INFORMATION:
 7
 8         (i)    APPLICANT:   Opperman, Hermann
 9                             Ozkaynak, Engin
10                             Rueger, David C.
11                             Kuberasampath, Thangavel
12         (ii)   TITLE OF INVENTION:  Osteogenic Proteins
13         (iii)  NUMBER OF SEQUENCES:   11
14         (iv)   CORRESPONDENCE ADDRESS:
15                (A) ADDRESSEE:  Testa Hurwitz & Thibeault
16                (B) STREET:  53 State Street
17                (C) CITY:  Boston
18                (D) STATE:  Massachusetts
19                (E) COUNTRY:  U.S.A.
20                (F) ZIP:  02109
21         (v)    COMPUTER READABLE FORM:
22                (A) MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
23                (B) COMPUTER:  IBM XT
24                (C) OPERATING SYSTEM:  DOS 3.30
25                (D) SOFTWARE:  ASC II
26         (vi)   CURRENT APPLICATION DATA:
27                (A) APPLICATION NUMBER: US 07/599,543
28                (B) FILING DATE:   18-Oct-90
29         (vii)  PRIOR APPLICATION DATA:
30                (A) APPLICATION NUMBER:  US 569,920
31                (B) FILING DATE:   20-Aug-90
32                (C) APPLICATION NUMBER:  US 315,342
33                (D) FILING DATE:   23-Feb-89
34                (E) APPLICATION NUMBER:  US 422,699
35                (F) FILING DATE:   17-Oct-89
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
```

**Does not comply
- Send a notice -**

insert
(C) CLASSIFICATION:

```
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71  (2)    INFORMATION FOR SEQ ID NO:1:
72         (i)    SEQUENCE CHARACTERISTICS:
73                (A) LENGTH:   139 amino acids
74                (B) TYPE:   amino acid
75                (D) TOPOLOGY:   linear
76         (ii)   MOLECULE TYPE:   protein
77         (ix)   FEATURE:
78                (A) NAME:   mOP2 (mature)
79         (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:1:
80
81  Ala  Ala  Arg  Pro  Leu  Lys  Arg  Arg  Gln
82    1                  5
83  Pro  Lys  Lys  Thr  Asn  Glu  Leu  Pro  His
84   10                      15
85  Pro  Asn  Lys  Leu  Pro  Gly  Ile  Phe  Asp
86        20                      25
87  Asp  Gly  His  Gly  Ser  Arg  Gly  Arg  Glu
88        30                          35
89  Val  Cys  Arg  Arg  His  Glu  Leu  Tyr  Val
90             40                          45
91  Arg  Phe  Arg  Asp  Leu  Gly  Trp  Leu  Asp
92                  50
93  Trp  Val  Ile  Ala  Pro  Gln  Gly  Tyr  Ser
94   55                  60
95  Ala  Tyr  Tyr  Cys  Glu  Gly  Glu  Cys  Ala
96        65                      70
97  Phe  Pro  Leu  Asp  Ser  Cys  Met  Asn  Ala
98             75                      80
99  Thr  Asn  His  Ala  Ile  Leu  Gln  Ser  Leu
100            85                          90
101 Val  His  Leu  Met  Lys  Pro  Asp  Val  Val
102                  95
103 Pro  Lys  Ala  Cys  Cys  Ala  Pro  Thr  Lys
104  100                 105
105 Leu  Ser  Ala  Thr  Ser  Val  Leu  Tyr  Tyr
106       110                     115
```

```
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137  Asp  Ser  Ser  Asn  Asn  Val  Ile  Leu  Arg
138            120                      125
139  Lys  His  Arg  Asn  Met  Val  Val  Lys  Ala
140            130                           135
141  Cys  Gly  Cys  His
142
143
144  (2)   INFORMATION FOR SEQ ID NO:2:
145        (i)    SEQUENCE CHARACTERISTICS:
146               (A) LENGTH:  1930 base pairs
147               (B) TYPE:  nucleic acid
148               (C) STRANDEDNESS:  single
149               (D) TOPOLOGY:  linear
150        (ii)   MOLECULE TYPE:  cDNA
151        (iii)  HYPOTHETICAL:  no
152        (iv)   ANTI-SENSE:  no
153        (vi)   ORIGINAL SOURCE:
154               (A) ORGANISM:  mouse
155               (F) TISSUE TYPE:  embryo
156        (ix)   FEATURE:
157               (A) NAME:  mOP2
158        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:2:
159
```

```
160  GGAATTCCGC TGCCAGGCAC AGGTGCGCCG TCTGGTCCTC    40
161  CCCGTCTGGC GTCAGCCGAG CCCGACCAGC TACCAGTGGA    80
162  TGCGCGCCGG CTGAAAGTCC GAG ATG GCT ATG CGT     115
163                              Met Ala Met Arg
164                               1
165  CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG    148
166  Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu
167   5                10                    15
168  TGC GCG CTG GGA GGC GGC CAC GGT CCC GGT CCC    181
169  Cys Ala Leu Gly Gly Gly His Gly Pro Gly Pro
170                   20                  25
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202  CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA GCG    214
203  Pro His Thr Cys Pro Gln Arg Arg Leu Gly Ala
204               30                  35
205  CGC GAC CGG GAC ATG CAG CGT GAA ATC CTG CCG    247
206  Arg Asp Arg Asp Met Gln Arg Glu Ile Leu Pro
207           40                  45
208  GTG CTC GGG CTA CCG GGA CGC CCC GAC CCC GTG    280
209  Val Leu Gly Leu Pro Gly Arg Pro Asp Pro Val
210       50                  55
211  CAC AAC CCG CCG CTG CCC GGC ACG CAG CGT GCG    313
212  His Asn Pro Pro Leu Pro Gly Thr Gln Arg Ala
```

```
213    60                       65                      70
214    CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG    346
215    Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met
216                            75                      80
217    ACC GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT    379
218    Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala
219                    85                      90
220    CAC TTA GGC CGT GCC GAC CTG GTC ATG AGC TTC    412
221    His Leu Gly Arg Ala Asp Leu Val Met Ser Phe
222              95                      100
223    GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC    445
224    Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly
225         105                     110
226    TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT    478
227    Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe
228    115                     120                     125
229    GAC CTA ACC CAG ATC CCT GCT GGG GAG GCT GTC    511
230    Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val
231                    130                     135
232    ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA CCC    544
233    Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu Pro
234              140                     145
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
```

```
266
267    AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC      577
268    Ser Thr His Pro Leu Asn Thr Thr Leu His Ile
269            150                 155
270    AGC ATG TTC GAA GTG GTC CAA GAG CAC TCC AAC      610
271    Ser Met Phe Glu Val Val Gln Glu His Ser Asn
272            160                 165
273    AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG      643
274    Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln
275    170                 175                 180
276    ACG CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG      676
277    Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val
278                    185                 190
279    CTG GAC ATC ACA GCA GCC AGT GAC CGA TGG CTG      709
280    Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu
281            195                 200
282    CTG AAC CAT CAC AAG GAC CTG GGA CTC CGC CTC      742
283    Leu Asn His His Lys Asp Leu Gly Leu Arg Leu
284            205                 210
285    TAT GTG GAA ACC GCG GAT GGG CAC AGC ATG GAT      775
286    Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp
287            215                 220
288    CCT GGC CTG GCT GGT CTG CTT GGA CGA CAA GCA      808
289    Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala
290    225                 230                 235
291    CCA CGC TCC AGA CAG CCT TTC ATG GTA ACC TTC      841
292    Pro Arg Ser Arg Gln Pro Phe Met Val Thr Phe
293                    240                 245
294    TTC AGG GCC AGC CAG AGT CCT GTG CGG GCC CCT      874
295    Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro
296            250                 255
297    CGG GCA GCG AGA CCA CTG AAG AGG AGG CAG CCA      907
298    Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro
299            260                 265
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
```

```
319
320
321
322
323
324
325
326
327
328
329
330
331
332   AAG AAA ACG AAC GAG CTT CCG CAC CCC AAC AAA    940
333   Lys Lys Thr Asn Glu Leu Pro His Pro Asn Lys
334       270                 275
335   CTC CCA GGG ATC TTT GAT GAT GGC CAC GGT TCC    973
336   Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser
337   280                 285                 290
338   CGC GGC AGA GAG GTT TGC CGC AGG CAT GAG CTC   1006
339   Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu
340                   295                 300
341   TAC GTC AGA TTC CGT GAC CTT GGC TGG CTG GAC   1039
342   Tyr Val Arg Phe Arg Asp Leu Gly Trp Leu Asp
343               305                 310
344   TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC TAT   1072
345   Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr
346           315                 320
347   TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC   1105
348   Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp
349       325                 330
350   TCC TGT ATG AAC GCC ACC AAC CAT GCC ATC TTG   1138
351   Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu
352   335                 340                 345
353   CAG TCT CTG GTG CAC CTG ATG AAG CCA GAT GTT   1171
354   Gln Ser Leu Val His Leu Met Lys Pro Asp Val
355                   350                 355
356   GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG   1204
357   Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu
358               360                 365
359   AGT GCC ACC TCT GTG CTG TAC TAT GAC AGC AGC   1237
360   Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser
361               370                 375
362   AAC AAT GTC ATC CTG CGT AAA CAC CGT AAC ATG   1270
363   Asn Asn Val Ile Leu Arg Lys His Arg Asn Met
364       380                 385
365
366
367
368
369
370
371
```

```
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397   GTG GTC AAG GCC TGT GGC TGC CAC                  1294
398   Val Val Lys Ala Cys Gly Cys His
399   390                     400
400   TGAGGCCCCG CCCAGCATCC TGCTTCTACT ACCTTACCAT      1334
401   CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT      1374
402   TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT      1414
403   CCCCTGGCCA CTTCCTGCTA AAATTCTGGT CTTTCCCAGT      1454
404   TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGCC      1494
405   CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC      1534
406   AGCATCCCAG AGCTATGCTA ACTGAGAGGT CTGGGGTCAG      1574
407   CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC      1614
408   CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGCC      1654
409   CTGGAATTCT AAACTAGATG ATCTGGGCTC TCTGCACCAT      1694
410   TCATTGTGGC AGTTGGGACA TTTTTAGGTA TAACAGACAC      1734
411   ATACACTTAG ATCAATGCAT CGCTGTACTC CTTGAAATCA      1774
412   GAGCTAGCTT GTTAGAAAAA GAATCAGAGC CAGGTATAGC      1814
413   GGTGCATGTC ATTAATCCCA GCGCTAAAGA GACAGAGACA      1854
414   GGAGAATCTC TGTGAGTTCA AGGCCACATA GAAAGAGCCT      1894
415   GTCTCGGGAG CAGGAAAAAA AAAAAAAACG GAATTC          1930
416
417
418   (2)   INFORMATION FOR SEQ ID NO:3:
419         (i)    SEQUENCE CHARACTERISTICS:
420                (A) LENGTH:  139 amino acids
421                (B) TYPE:  amino acid
422                (D) TOPOLOGY:  linear
423         (ii)   MOLECULE TYPE:  protein
424         (ix)   FEATURE:
```

```
425                  (A) NAME:   hOP2 (mature)
426           (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:3:
427
428   Ala  Val  Arg  Pro  Leu  Arg  Arg  Arg  Gln
429    1                   5
430   Pro  Lys  Lys  Ser  Asn  Glu  Leu  Pro  Gln
431    10                      15
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464   Ala  Asn  Arg  Leu  Pro  Gly  Ile  Phe  Asp
465         20                  25
466   Asp  Val  His  Gly  Ser  His  Gly  Arg  Gln
467         30                  35
468   Val  Cys  Arg  Arg  His  Glu  Leu  Tyr  Val
469              40                       45
470   Ser  Phe  Gln  Asp  Leu  Gly  Trp  Leu  Asp
471                   50
472   Trp  Val  Ile  Ala  Pro  Gln  Gly  Tyr  Ser
473    55                  60
474   Ala  Tyr  Tyr  Cys  Glu  Gly  Glu  Cys  Ser
475         65                  70
476   Phe  Pro  Leu  Asp  Ser  Cys  Met  Asn  Ala
477         75                       80
```

```
478  Thr  Asn  His  Ala  Ile  Leu  Gln  Ser  Leu
479                      85                      90
480  Val  His  Leu  Met  Lys  Pro  Asn  Ala  Val
481                      95
482  Pro  Lys  Ala  Cys  Cys  Ala  Pro  Thr  Lys
483  100                      105
484  Leu  Ser  Ala  Thr  Ser  Val  Leu  Tyr  Tyr
485       110                      115
486  Asp  Ser  Ser  Asn  Asn  Val  Ile  Leu  Arg
487       120                           125
488  Lys  Ala  Arg  Asn  Met  Val  Val  Lys  Ala
489            130                           135
490  Cys  Gly  Cys  His
491
492
493  (2)   INFORMATION FOR SEQ ID NO:4:
494        (i)   SEQUENCE CHARACTERISTICS:
495              (A) LENGTH: 1956 base pairs     only 1941 are listed
496              (B) TYPE:  nucleic acid           See line 797
497              (C) STRANDEDNESS:  single
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529              (D) TOPOLOGY:  linear
530        (ii)  MOLECULE TYPE:  cDNA
```

```
531      (iii) HYPOTHETICAL:  no
532      (iv)  ANTI-SENSE:  no
533      (vi)  ORIGINAL SOURCE:
534            (A) ORGANISM:  homo sapiens
535            (F) TISSUE TYPE:  hippocampus
536      (ix)  FEATURE:
537            (A) NAME: hOP2
538      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:4:
539
540  GGAATTCCGG CCACAGTGGC GCCGGCAGAG CAGGAGTGGC      40
541  TGGAGGAGCT GTGGTTGGAG CAGGAGGTGG CACGGCAGGG      80
542  CTGGAGGGCT CCCTATGAGT GGCGGAGACG GCCCAGGAGG     120
543  CGCTGGAGCA ACAGCTCCCA CACCGCACCA AGCGGTGGCT     160
544  GCAGGAGCTC GCCCATCGCC CCTGCGCTGC TCGGACCGCG     200
545  GCCACAGCCG GACTGGCGGG TACGGCGGCG ACAGAGGCAT     240
546  TGGCCGAGAG TCCCAGTCCG CAGAGTAGCC CCGGCCTCGA     280
547  GGCGGTGGCG TCCCGGTCCT CTCCGTCCAG GAGCCAGGAC     320
548  AGGTGTCGCG CGGCGGGGCT CCAGGGACCG CGCCTGAGGC     360
549  CGGCTGCCCG CCCGTCCCGC CCCGCCCCGC CGCCCGCCGC     400
550  CCGCCGAGCC CAGCCTCCTT GCCGTCGGGG CGTCCCCAGG     440
551  CCCTGGGTCG GCCGCGGAGC CGATGCGCGC CCGCTGAGCG     480
552  CCCCAGCTGA GCGCCCCCGG CCTGCC ATG ACC GCG CTC    518
553                                 Met Thr Ala Leu
554                                  1
555  CCC GGC CCG CTC TGG CTC CTG GGC CTG GCG CTA    551
556  Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu
557   5               10                     15
558  TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA    584
559  Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg
560                       20                25
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
```

```
584
585
586
587
588
589
590
591
592
593
594   CCC CCG CCC GGC TGT CCC CAG CGA CGT CTG GGC     617
595   Pro Pro Pro Gly Cys Pro Gly arg Arg Leu Gly
596                30                  35
597   GCG CGC GAC CGG GAC GTG CAG CGC GAG ATC CTG     650
598   Ala Arg Asp Arg Asp Val Gln Arg Glu Ile Leu
599                40                  45
600   GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC     683
601   Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro
602        50                  55
603   CGC GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG     716
604   Arg Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala
605   60                  65                  70
606   TCC GCG CCG CTC TTC ATG CTG GAC CTG TAC CAC     749
607   Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His
608                75                  80
609   CGC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCC     782
610   Arg Met Ala Gly Asp Asp Asp Glu Asp Gly Ala
611                85                  90
612   GCG GAG GCC CTG GGC CGC GCC GAC CTG GTC ATG     815
613   Ala Glu Ala Leu Gly Arg Ala Asp Leu Val Met
614                95                  100
615   AGC TTC GTT AAC ATG GTG GAG CGA GAC CGT GCC     848
616   Ser Phe Val Asn Met Val Glu Arg Asp Arg Ala
617        105                 110
618   CTG GGC CAC CAG GAG CCC CAT TGG AAG GAG TTC     881
619   Leu Gly His Gln Glu Pro His Trp Lys Glu Phe
620   115                 120                 125
621   CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG     914
622   Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu
623                130                 135
624   GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG     947
625   Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys
626                140                 145
627
628
629
630
631
632
633
634
635
636
```

```
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659    GTG CCC AGC ATC CAC CTG CTC AAC AGG ACC CTC    980
660    Val Pro Ser Ile His Leu Leu Asn Arg Thr Leu
661            150                 155
662    CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG    1013
663    His Val Ser Met Phe Gln Val Val Gln Glu Gln
664        160                 165
665    TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT    1046
666    Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp
667    170                 175                 180
668    CTT CAG ACG CTC CGA GCT GGA GAC GAG GGC TGG    1079
669    Leu Gln Thr Leu Arg Ala Gly Asp Glu Gly Trp
670                185                 190
671    CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC    1112
672    Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys
673                195                 200
674    TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC    1145
675    Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu
676                205                 210
677    CGC CTC TAT GTG GAG ACT GAG GAC GGG CAC AGC    1178
678    Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser
679        215                 220
680    GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT CAA    1211
681    Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln
682    225                 230                 235
683    CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC    1244
684    Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val
685                240                 245
686    ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC    1277
687    Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg
688                250                 255
689    ACC CCT CGG GCA GTG AGG CCA CTG AGG AGG AGG    1310
```

```
690   Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg
691           260             265
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724   CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC   1343
725   Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala
726       270             275
727   AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC   1376
728   Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His
729   280             285                 290
730   GGC TCC CAC GGC CGG CAG GTC TGC CGT CGG CAC   1409
731   Gly Ser His Gly Arg Gln Val Cys Arg Arg His
732               295                 300
733   GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG   1442
734   Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp
735           305             310
736   CTG GAC TGG GTC ATC GCT CCC CAA GGC TAC TCG   1475
737   Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser
738           315             320
739   GCC TAT TAC TGT GAG GGG GAG TGC TCC TTC CCA   1508
740   Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro
741       325             330
742   CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC   1541
```

```
743  Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
744  335                 340                 345
745  ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA   1574
746  Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
747                  350                 355
748  AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC   1607
749  Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr
750                  360                 365
751  AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC   1640
752  Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
753                  370                 375
754  AGC AGC AAC AAC GTC ATC CTG CGC AAA GCC CGC   1673
755  Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg
756      380                 385
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789  AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC       1703
790  Asn Met Val Val Lys Ala Cys Gly Cys His
791  390                 395
792  TGAGTCAGCC CGCCCAGCCC TACTGCAGCA ATTCACTGGC   1743
793  CGTCGTTTTA CAACGTGTGA CTGGGAAAAC CCTGGCGTTA   1783
794  CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG   1823
795  CTGGCTAATA GCGAAGAGGC CCCGCACCGA TCGCCCTTCC   1863
```

```
796    CAACAGTTGC GCCCCAGTGA ATGGCGAATG GCAAATTGTA  1903
797    AGCGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTT    (1941)  see line 495
798
799
800    (2)    INFORMATION FOR SEQ ID NO:5:
801           (i)     SEQUENCE CHARACTERISTICS:
802                   (A) LENGTH:  98 amino acids
803                   (B) TYPE:  amino acid
804                   (D) TOPOLOGY:  linear
805           (ii)   MOLECULE TYPE:  protein
806           (ix)   FEATURE:
807                   (D) OTHER INFORMATION: wherein "res."
808    means "residue" and Xaa at res. 2 = (Lys or Arg); Xaa at
809    res.3 = (Lys or Arg); Xaa res.9 = (Ser or Arg); Xaa at
810    res.11 = (Arg or Gln); Xaa at res.16 = (Gln or Leu); Xaa
811    at res. 19 = (Ile or Val); Xaa at res.23 = (Glu or Gln);
812    Xaa at res.26 = (Ala or Ser); Xaa at res. 34 = (Ala or
813    or Ser); Xaa at res.38= (Asn or Asp); Xaa at res. 40 =
814    (Tyr or Cys); Xaa at res.49 = (Val or Leu); Xaa at
815    res.52= (His or Asn); Xaa at res. 53 = (Phe or
816    Leu); Xaa at res. 54 = (Ile or Met); Xaa at res. 55 = (Asn
817    or Lys); Xaa at res. 56 = (Glu, Asp or Asn); Xaa at res.
818    57=(Thr, Ala or Val); Xaa at res. 61 = (Pro or Ala);
819    Xaa at res. 67=(gln or Lys); Xaa at res. 69 =
820    (Asn or Ser); Xaa at 71=(Ile or Thr); Xaa at res.
821    76= (Phe or Tyr); Xaa at res. 78 = (Asp, Glu or Ser);
822    Xaa at res. 80= (Ser or Asn); Xaa at res. 84 = (Ile or
823    Asp); Xaa at res. 85 Arg); Xaa at res. 87 = (Tyr, Ala
824    or His); and Xaa at res. 93=(Arg or Lys)
825
826           (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:5:
827
828    Cys Xaa  Xaa  His Glu Leu Tyr Val Xaa  Phe
829     1                5                    10
830    Xaa  Asp Leu Gly Trp Xaa  Asp Trp Xaa  Ile
831                     15                    20
832    Ala Pro Xaa  Gly Tyr Xaa  Ala Tyr Tyr Cys
833                     25                    30
834    Glu Gly Cys Xaa  Phe Pro Leu Xaa   Ser Xaa
835                     35                    40
836    Met Asn Ala Thr Asn His Ala Ile Xaa   Thr
837                     45                    50
838    Leu Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Val
839                         55
840    Pro Lys Xaa   Cys Cys Ala Pro Thr Xaa   Leu
841         60                    65
842
843
844
845
846
847
848
```

```
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874     Xaa     Ala Xaa     Ser Val Leu Tyr Xaa     Asp
875             70                      75
876     Xaa     Ser Xaa     Asn Val Xaa     Leu Xaa     Lys
877             80                      85
878     Xaa     Pro Asn Met Val Val Xaa     Ala Cys Gly
879             90                      95
880     Cys His
881
882
883  (2)   INFORMATION FOR SEQ ID NO:6:
884        (i)    SEQUENCE CHARACTERISTICS:
885               (A) LENGTH:  437 base pairs
886               (B) TYPE:  nucleic acid
887               (C) STRANDEDNESS:  single
888               (D) TOPOLOGY:  linear
889        (ii)   MOLECULE TYPE:  cDNA
890        (iii)  HYPOTHETICAL:  no
891        (iv)   ANTI-SENSE:  no
892        (vi)   ORIGINAL SOURCE:
893
894
895
896
897
898
899
900
901
```

```
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921            (A) ORGANISM:  Human
922            (F) TISSUE TYPE:  placenta
923      (ix)  FEATURE:
924            (A) NAME:  OP1
925      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:6:
926
927                                          TCC ACG GGG      9
928                                          Ser Thr Gly
929                                           1
930  AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG        42
931  Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr
932   5                    10
933  CCC AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC        75
934  Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn
935  15                    20                  25
936  GTG GCA GAG AAC AGC AGC AGC GAC CAG AGG CAG        108
937  Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln
938                    30                  35
939  GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC        141
940  Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
941                40                  45
942  CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG        174
943  Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
944            50                  55
945  CCT GAA GGC TAC GCC GCC TAC TAC TGT GAG GGG        207
946  Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly
947        60                  65
948  GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC        240
949  Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
950  70                    75                  80
951  GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC        273
952  Ala Thr Asn His Ala Ile Val Gln Thr Leu Val
953                85                  90
954
```

```
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986    CAC TTC ATC AAC CCG GAA ACG GTG CCC AAG CCC        306
987    His Phe Ile Asn Pro Glu Thr Val Pro Lys Pro
988                    95                  100
989    TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC        339
990    Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser
991            105                  110
992    GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC        372
993    Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
994        115                  120
995    CTG AAG AAA TAC AGA AAC ATG GTG GTC CGG GCC        405
996    Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala
997    125                  130                  135
998    TGT GGC TGC CAC TAGCTCCTCC GAGAATTCAG              437
999    Cys Gly Cys His
1000
1001
1002   (2)    INFORMATION FOR SEQ ID NO:7:
1003          (i)    SEQUENCE CHARACTERISTICS:
1004                 (A) LENGTH:  102 amino acids
1005                 (B) TYPE:  amino acid
1006                 (D) TOPOLOGY:  linear
1007          (ii)   MOLECULE TYPE:  protein
```

Patent Application US/07/599,543B

```
1008        (ix)  FEATURE:
1009              (D) OTHER INFORMATION:
1010   wherein each Xaa independently represents one of
1011   the 20 naturally occurring L-isomer, a-amino acids.
1012
1013        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:7:
1014
1015   Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1016    1               5                   10
1017   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1018                  15                  20
1019   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
1020                  25                  30
1021   Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1022           35                  40
1023   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1024   45                      50                  55
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1057                  60                  65
1058   Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1059                  70                  75
1060   Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
```

```
1061                     80                      85
1062        Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1063              90                      95
1064        Xaa Cys Xaa
1065        100
1066
1067    (2)    INFORMATION FOR SEQ ID NO:8:
1068           (i)     SEQUENCE CHARACTERISTICS:
1069                   (A) LENGTH:  97 amino acids
1070                   (B) TYPE:  amino acid
1071                   (D) TOPOLOGY:  linear
1072           (ii)   MOLECULE TYPE:  protein
1073           (ix)   FEATURE:
1074                   (D) OTHER INFORMATION:
1075    wherein each Xaa independently represents one of
1076    the 20 naturally occurring L-isomer, a-amino acids
1077
1078           (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:8:
1079
1080        Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1081         1               5                    10
1082        Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1083                       15                    20
1084        Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1085                       25                    30
1086        Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1087              35                    40
1088        Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1089         45                    50                    55
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
```

```
1114
1115
1116
1117
1118
1119
1120
1121
1122      Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa
1123                      60                  65
1124      Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1125                  70                  75
1126      Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1127              80                  85
1128      Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa
1129          90                  95
1130
1131
1132  (2)      INFORMATION FOR SEQ ID NO:9:
1133          (i)   SEQUENCE CHARACTERISTICS:
1134              (A)   LENGTH: 136 amino acids
1135              (B)   TYPE:  amino acid
1136              (D)   TOPOLOGY:  linear
1137          (ii) MOLECULE TYPE:  protein
1138          (ix) FEATURE:
1139              (A) NAME: hOP-2P
1140          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
1141
1142              Pro  Leu  Arg  Arg  Arg  Gln
1143               1                   5
1144  Pro  Lys  Lys  Ser  Asn  Glu  Leu  Pro  Gln
1145           10                       15
1146  Ala  Asn  Arg  Leu  Pro  Gly  Ile  Phe  Asp
1147                   20
1148  Asp  Val  Asn  Gly  Ser  His  Gly  Arg  Gln
1149   25                   30
1150  Val  Cys  Arg  Arg  His  Glu  Leu  Tyr  Val
1151       35                   40
1152  Ser  Phe  Gln  Asp  Leu  Gly  Trp  Leu  Asp
1153           45                   50
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
```

1220	Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
1221		5					10		
1222									
1223									
1224									
1225									
1226									
1227									
1228									
1229									
1230									
1231									
1232									
1233									
1234									
1235									
1236									
1237									
1238									
1239									
1240									
1241									
1242									
1243									
1244									
1245									
1246									
1247									
1248									
1249									
1250									
1251									
1252									
1253	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
1254			15					20	
1255	Asp	Val	Asn	Gly	Ser	His	Gly	Arg	Gln
1256			25						30
1257	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
1258					35				
1259	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
1260	40					45			
1261	Tyr	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
1262		50					55		
1263	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
1264			60					65	
1265	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
1266				70					75
1267	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
1268					80				
1269	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
1270	85					90			
1271	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
1272		95					100		

```
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186    Tyr  Val  Ile  Ala  Pro  Gln  Gly  Tyr  Ser
1187                   55                       60
1188    Ala  Tyr  Tyr  Cys  Glu  Gly  Glu  Cys  Ser
1189                        65
1190    Phe  Pro  Leu  Asp  Ser  Cys  Met  Asn  Ala
1191    70                      75
1192    Thr  Asn  His  Ala  Ile  Leu  Gln  Ser  Leu
1193         80                      85
1194    Val  His  Leu  Met  Lys  Pro  Asn  Ala  Val
1195              90                      95
1196    Pro  Lys  Ala  Cys  Cys  Ala  Pro  Thr  Lys
1197                   100                      105
1198    Leu  Ser  Ala  Thr  Ser  Val  Leu  Tyr  Tyr
1199                        110
1200    Asp  Glu  Ser  Asn  Asn  Val  Ile  Leu  Arg
1201    115                      120
1202    Lys  Ala  Arg  Asn  Met  Val  Val  Lys  Ala
1203         125                      130
1204    Cys  Gly  Cys  His
1205              135
1206
1207
1208    (2)     INFORMATION FOR SEQ ID NO:10:
1209            (i)  SEQUENCE CHARACTERISTICS:
1210                 (A)  LENGTH: 133 amino acids
1211                 (B)  TYPE:  amino acid
1212                 (D)  TOPOLOGY:  linear
1213            (ii) MOLECULE TYPE:  protein
1214            (ix) FEATURE:
1215                 (A) NAME: hOP-2R
1216            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
1217
1218                                  Arg  Arg  Gln
1219                                   1
```

[handwritten annotation at line 1204: "⊘ not valid, please delete"]

```
1273  Leu  Ser  Ala  Thr  Ser  Val  Leu  Tyr  Tyr
1274            105                      110
1275  Asp  Glu  Ser  Asn  Asn  Val  Ile  Leu  Arg
1276            115                           120
1277  Lys  Ala  Arg  Asn  Met  Val  Val  Lys  Ala
1278                      125
1279  Cys  Gly  Cys  His◯ delete
1280  130
1281
1282
1283  (2)       INFORMATION FOR SEQ ID NO:11:
1284            (i)   SEQUENCE CHARACTERISTICS:
1285                  (A)  LENGTH: ⟨170 amino acids⟩ 160
1286                  (B)  TYPE:  amino acid
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317                  (D)  TOPOLOGY:  linear
1318            (ii)  MOLECULE TYPE:  protein
1319            (ix)  FEATURE:
1320                  (A) NAME: hOP-2S
1321            (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:11:
1322
1323                                Ser  Gln  Gln
1324                                 1
1325  Pro  Phe  Val  Val  Thr  Phe  Phe  Arg  Ala
```

1326		5				10		
1327	Ser	Pro	Ser	Pro	Ile	Arg	Thr	Pro	Arg
1328			15					20	
1329	Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
1330				25					30
1331	Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
1332					35				
1333	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
1334	40					45			
1335	Asp	Val	Asn	Gly	Ser	His	Gly	Arg	Gln
1336		50					55		
1337	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
1338			60					65	
1339	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
1340				70					75
1341	Tyr	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
1342					80				
1343	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
1344	85					90			
1345	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
1346		95					100		
1347	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
1348			105					110	
1349	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
1350				115					120
1351	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
1352					125				

1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378

```
1379
1380
1381
1382
1383
1384    Leu   Ser   Ala   Thr   Ser   Val   Leu   Tyr   Tyr
1385    130                           135
1386    Asp   Glu   Ser   Asn   Asn   Val   Ile   Leu   Arg
1387          140                           145
1388    Lys   Ala   Arg   Asn   Met   Val   Val   Lys   Ala
1389                150                           165
1390    Cys   Gly   Cys   His
1391                      170          155
1392
1393                      160
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
```

1432
1433
1434

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/599,543B

LINE ERROR   ORIGINAL TEXT

27	Wrong application Serial Number	*ok* → (A) APPLICATION NUMBER: US 07/599,543
538	Entered and Calc. Seq. Length differ	*see p.15* → (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
811	Response Exceeds Line Limitations	at res. 19 = (Ile or Val); Xaa at res.23
812	Response Exceeds Line Limitations	Xaa at res.26 = (Ala or Ser); Xaa at res
813	Response Exceeds Line Limitations	or Ser); Xaa at res.38= (Asn or Asp); Xa
814	Response Exceeds Line Limitations	*4 line* (Tyr or Cys); Xaa at res.49 = (Val or Le
815	Response Exceeds Line Limitations	*limit,* res.52= (His or Asn); Xaa at res. 53 = (
816	Response Exceeds Line Limitations	*but o.k.* Leu); Xaa at res. 54 = (Ile or Met); Xaa
817	Response Exceeds Line Limitations	*here* or Lys); Xaa at res. 56 = (Glu, Asp or A
818	Response Exceeds Line Limitations	57=(Thr, Ala or Val); Xaa at res. 61 = (
819	Response Exceeds Line Limitations	Xaa at res. 67=(gln or Lys); Xaa at res.
820	Response Exceeds Line Limitations	(Asn or Ser); Xaa at 71=(Ile or Thr); Xa
821	Response Exceeds Line Limitations	76= (Phe or Tyr); Xaa at res. 78 = (Asp,
822	Response Exceeds Line Limitations	Xaa at res. 80= (Ser or Asn); Xaa at res
823	Response Exceeds Line Limitations	Asp); Xaa at res. 85 Arg); Xaa at res. 8
824	Response Exceeds Line Limitations	or His); and Xaa at res. 93=(Arg or Lys)
1204	Wrong Amino Acid Designator	Cys Gly Cys His *delete*
1140	Entered and Calc. Seq. Length differ *error due to*	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
1279	Wrong Amino Acid Designator	Cys Gly Cys His *O*
1216	Entered and Calc. Seq. Length differ *error due to*	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
1321	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/599,543B

MANDATORY IDENTIFIER THAT WAS NOT FOUND

CLASSIFICATION

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/599,543B

LINE	ORIGINAL TEXT	CORRECTED TEXT
78	(A) NAME: mOP2 (mature)	(A) NAME/KEY: mOP2 (mature)
157	(A) NAME: mOP2	(A) NAME/KEY: mOP2
425	(A) NAME: hOP2 (mature)	(A) NAME/KEY: hOP2 (mature)
537	(A) NAME: hOP2	(A) NAME/KEY: hOP2
924	(A) NAME: OP1	(A) NAME/KEY: OP1
1139	(A) NAME: hOP-2P	(A) NAME/KEY: hOP-2P
1215	(A) NAME: hOP-2R	(A) NAME/KEY: hOP-2R
1320	(A) NAME: hOP-2S	(A) NAME/KEY: hOP-2S